

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp.fastaCAAQPaiHi: 995 aa  
>SEQ ID NO:2  
vs /tmp.fastaDAARPaiHi library  
searching /tmp.fastaDAARPaiHi library

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 39, opt: 27, gap-pen: -12/ -2, width: 16  
Scan time: 0.050  
The best scores are: opt  
NM\_000096 ACCESSION:NM\_000096 NID: gi 4557484 ref (1008) 2671  
>>NM\_000096 ACCESSION:NM\_000096 NID: gi 4557484 ref NM\_0 (1008 aa)  
initn: 1414 init1: 972 opt: 2671  
Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

	10	20	30	40	50	
SEQ	MKILILGIFLFLCSSPGWAIDRHCYIGIEESIWNYAPSGKNMLNEKPFSEDLE---FLQ	.....	.....	.....	.....	.....
NM_000	MKILILGIFLFLCSTPAWAKEKHYYIGIIETTWDYA---SDHGEKKLISVDTEHSNIYLQ	.....	.....	.....	.....	.....
	10	20	30	40	50	
SEQ	GGQARKSFVFKKALYFQYTDNTFQRRIIEKPSWLGFGLGPMIKAETGDFIYVHVKNNASRAY	.....	.....	.....	.....	.....
NM_000	NGPDRIGRLYKKALYLQYTDETFRRTIEKPVWLGFGLGPIIKAETGDKVYVHLKNLASRPY	.....	.....	.....	.....	.....
	60	70	80	90	100	110
SEQ	SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWYVEEHQGPGPNDSNCV	.....	.....	.....	.....	.....
NM_000	TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCV	.....	.....	.....	.....	.....
	120	130	140	150	160	170
SEQ	TRIYHSHIDTARDVASGLIGPLITCKRGTLNGDTEKDIDRSSFLMFSTTDESRSWYSDEN	.....	.....	.....	.....	.....
NM_000	TRIYHSHIDAPKDIASGLIGPLIICKKDSLKEKEKHIDREFVVMFSVVVDENFSWYLEDN	.....	.....	.....	.....	.....
	180	190	200	210	220	230
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMCAEDRVQWYFVGGMGVADIH	.....	.....	.....	.....	.....
NM_000	IKTYCSEPEKVDKDNEDFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFGMGNEDVH	.....	.....	.....	.....	.....
	240	250	260	270	280	290
SEQ	PVYLRGQTLISRNHRKDTIMLFPSLEDAFMVAKAPGVWMLGCQ---IHESMQAFFKVS	.....	.....	.....	.....	.....
NM_000	AAFFHGQALTNKNYRIDTINLFATLFDAYMVAQNPGEWMLSQNLNHLKAGLQAFFQVQ	.....	.....	.....	.....	.....
	300	310	320	330	340	350
SEQ	300 310 320 330 340 350	.....	.....	.....	.....	.....
NM_000	300 310 320 330 340 350	.....	.....	.....	.....	.....

	360	370	380	390	400	410
SEQ	NCQKPSTEAFVTGTHVIHYYIAAKEILWNYAPSGIDFFTKKNLTAAGSKSQLFFERSPTR					
NM_000	ECNKSSSKDNIRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQQGTTTR					
	360	370	380	390	400	410
	420	430	440	450	460	
SEQ	IGGYKLLIYREYTDASFQTQKAR---EEHLGLGPVFKAEVGQTIKITFYNNASLPLSI					
NM_000	IGGSYKKLVYREYTDASFNTNRKERGPEEEHLGLGPVIWAEVGDTIRVTFHNGAYPLSI					
	420	430	440	450	460	470
	470	480	490	500	510	520
SEQ	QPPGLHYNKSNEGLFYE---TPGG-STPPPSHVSPGTTFVYTWEPKDVGPTSTDPNCL					
NM_000	EPIGVRFNKNNEGTYYSPPNQSRSPVPSASHVAPTEFTYEWTVPKEVGPTNADPVCL					
	480	490	500	510	520	530
	530	540	550	560	570	580
SEQ	TWFYSSVNGKKDINSGLLGPLLICRNGSLGDDGKQKGVDKEFYLLATIFDENESNLDE					
NM_000	AKMYYSAVDPTKDIFTGLIGPMKICKKGSLHANGRQKDVDKEFYLFPTVFDENESLLED					
	540	550	560	570	580	590
	590	600	610	620	630	640
SEQ	N-RTFITEPENIDKEDTDCQASNKMYISINGYMYGNLPGLDTCLGDNVLWHVFSVGSVEDL					
NM_000	NIRMFTTAPDQVDKEDEDQFQESNKMHSMMNGFMYGNQPLTMCKGDSVVWYLFSGNEADV					
	600	610	620	630	640	650
	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSLGARRDTIPMFPTSQTLMPDSIGTFDLVCMTIKHNLGGMKHKYHV					
NM_000	HGIYFSGNTYLWRGERRDATANLFPQTSLTLMWPDTEGTFNVECLTTDHYTGGMKQKYTV					
	660	670	680	690	700	710
	710	720	730	740	750	760
SEQ	RQCQKPNPDQTQYQEEKIIITIAAEEMEDYSPSRKWENELHHLRRENQTSMYVDRSGTL					
NM_000	NQCRRQSEDSTFYLGERTYY-IIAAVEVWDYSPQREWEKELHHLQEQNVSNAFLDKGEFY					
	720	730	740	750	760	770
	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQYDDNTFTNQTKRNEGEKHLDILGPLILLNPGQIIQIIFKNKAARPYSI					
NM_000	IGSKYKKVYRQYTDSTFRVPVERKAEEEHLGILGPQLHADVGDKVKIIFKNMATRPySI					
	780	790	800	810	820	830
	830	840	850	860	870	880
SEQ	HAHGVTNNSTVVPTQPGEIQIYTQWQIPDRTGPTSLDFECIPWFYVSTSVAKDLHSGLV					
NM_000	HAHGVTESSTVTPTLPGETLTYVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLI					
	840	850	860	870	880	890

	890	900	910	920	930
SEQ	GPLSVCR	---KDINPN	-IVHRLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL		
	:::	:::	..:	.:.	.:.
NM_000	GPLIVCRRPYLKVFNPRRKLE	FALLFLVFDENESWYLDNNIKTYSDHPEKVNKDDEEFIE			
	900	910	920	930	940
	940	950	960	970	980
SEQ	SNQMHAINGRLFGNNQGITFHVGDVVNWYLIGIGNEADLHTVHFHGH	SFEYKHKYLI			
	::.	::.	::.	::.	::.
NM_000	SNKMHAINGRMFGNLQGLTMHGDEVNWYLMGMGNEIDLHTVHFHGH	FQYKHR			
	960	970	980	990	1000

995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:16:31 2002 done: Wed Sep 18 11:16:32 2002

Scan time: 0.050 Display time: 1.417

Function used was FASTA